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GenCore version 4.5 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: January 25, 2000, 03:59:51 ; search time 29.27 Seconds (without alignments) 546.229 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-332-063-2 3347 1 MPRAQPSSASYQPVPADPF1......KTPIQILGQEPDAEMVEYLI 675

Sea - hed: Scoring table: BLOSUM62 188963 seqs, 23686106 residues

ase : A_Geneseq_35:*

Word size :

Number of hits that pass the threshold :

188963

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ortebrococcus buen	ŧ	Human NonO/TEF3 for		Mycobacterium tube		TMF. New protein c	Human 160kb mediat	. Leishmania chagasi	Q.	eptococcus p		n protein se			g O	mDia Rho		_	once of the	chromosome			Antigen to-7a Vac	LexA/NuMA fusion p	GALA /HA /NIMA fileio	Rattile porvegions	Streptococcus ubor	Human mbia pho tar	Nucleolar Condocan	T. Cruzi LiyE homo		Trypanosoma cruzi	Kinetochore protei	mitosin a	mitosin	neural	e neural	ral Men	Description	•	

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109 FAS:AMITALEVLNSQ------EAGPTLPRONSQLPAQVQNGPSQEELEIQRRQL----- 148

148 - QUOORQKELERERMERERLEREFLERERLER-----ERLEQE--QLERQRQEREHVE 197

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Guary Match 6.9%; Store 229.5; DB 1; Length 783; Sest Local Similarity 20.7%; Prod. No. 1.5e-06; Putches 153; Conservative 63; Mismatches 205; Indels 221;

98 FNEDLRERLETANKQLAEKEYEGSEUTRKTISQLFA--KNKESQREKEKLEAELATARST 155

Gaps

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ALIGNMENTS

\$6383C	3888	8888	8888%	ুৰুমুগ্ৰ	7	PE PE	RESULT W37151 IP W AC W DE M EW N
drugs and therapeutic agents useful to evaluate and/or control cytoskelete' dynamic events involved in normal and abnormal cell morphology adhesion, motility, growth and/or differentiation. A mernod of detecting a modulator of Mena activity/expression is chaimed. Sequence 783 AA;	1.3508-59eClild distribution. Based on the disclosed Mena and Evl genes (see also V02996-97) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endocenous and exceeding.	mammalian Ena (Mena, see W37148). Two other isoforms, neural Mena++ (see W37152) and neural Mena+++ (see W37153), are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural	This protein comprises novel murine neural Mena+. Its amino acid sequence was deduced from a cDNA clone (see V02998) obtained from a mouse brain cDNA. Library. Neural Mena+ contains an excu that introduces 244 amino acids between amino acids and section and sections.	s of M ytoske gy, ad	1: .IN. 1998. (3UL-1997; U11669. (3UL-1996; US-675815. (3UL-1997) (3UL-199	cell motility; mouse. Location/Qualifiers ence 378 ence 478 encoded by GGF" 1.	JUT 1 .51 .51 .51 .51 .51 .51 .51 .51 .51 .5

EKDAMIKVLQQORSRKEPSKTEQLSCWRPAKSLMS] ::	PS Example 4: Page 63-65 CC This protein comprise CC sequence was deduced CC CDNA library. Two ot CC neural Mena++ (see W37 CC Ena (Mena, see W37)148 CC genes (see also V0299 CC variety of methods an CC drugs and therapeutic CC drugs and therapeutic CC drugs and therapeutic CC drugs and therapeutic CC morphology, adhesion, CC method of detecting a CC claimed. SQ Sequence 802 AA;	W37153 standa W37153; W37153; U6-JUL-1998 Mouse neural Neural Mena++ cytoskeleton; cell growth; Mus musculus. W09801755-A1. 15-JAN-1998. 15-JAN-1998. 15-JUL-1997; 05-JUL-1996; 10-7(GBFB) GES B. 3UTC-) HUTCH. JETT FE, N. WPI; 98-10119 Detection of i	490 TAATITY 401 PNGSLDS 521 ATAAATA 461 GTPLAST 574 -ALV 577 OGLVLGP 630 RLSIPSL 630 RDSPPPPP	Oy 336 EGRIKTLHAQIIE Db 283 Oy 394 STLTGSPIMEEKR Oy 392 ATVP-RPLNKNSR OY 43 SPVPPSTPLLSAH OY 43 SPVPPSTPLLSH OB 359 SPLPPSPPIMISS
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מו הוו מו או מו שו מו שו מו שו מו	Mena+++ I ained from a Mena+ (see W Mena+ (s	bled protein; Evon; cell differer en cell differer en cell differer en cell differer en cell e	PPPLPPPLASLSHGSQASPPPSAAAAAAVQVAPAAAAAPSPP SAAAAAAVQVAPAAAAAPAPVPAP	LSCMRPAKSLMSISNAGSGLLSHS

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                                                                                                                            05-JUL-1996; US-675815.
(GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
(HUTC-) HUTCHINSON CANCER RES CENT FRED.
GETCLET FB, Niebuhr K, Soriano P, Wehland J;
WPI; 98-101197/09.
                                                                                                                                                                                                                                                                                                        Mouse neural Mena++ protein.

Neural Mena++ protein; mammalian Ena; Enabled protein; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                  W37152;
06-JUL-1998 (first entry)
                                                                                Detection of modulators of Mena and Ena-VASP-like genes and proteins used in control of cytoskeletal dynamic events in normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                  W37152 standard; Protein; 787 AA.
                         Example 4; Page 60-63;
                                            ibnormal cell morphology, adhesion, motility, growth
                                                                                                                                                                                                                              )3-JUL-1997; U11669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 574 ----PSTGPPPPPPPPPPP----PNQAPPPPPPPPPPPAPPLPASGIFSGSTSEDNRPL 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            617 EVPASPATGPGPHRLSIPSLTCNPDKTDGP------
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      protein comprises
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77pp; English.
novel murine neural Mena++.
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Ena (Mena, see W37148), neural Mena isoforms exhibit neural
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                                    RLSIPSLTCNPDKTDGP--
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PPPPPPL---PNQAPPPPPPPPPPPLPASGIFSGSTSEDNRPL
                                                                      QGLVLGPPAPPPPPPPPPSGPAY----ASALPPPPGPPPPPPL
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                                                                                                                                                                                                                                                            TAATITTTMVAAAPVAVAAAAAP--
                                                                                                                                                                                                                                                                                                  SPLPPSPPIMISSPPGKATGPR--
                                                                                                                                                                                                                                                                                                                                                                                                       STLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPA--KSLMSISNAGSGLLSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRMSNAAPSSDSSLSSAPLPEYSSCQPESAPPPSYAKVISAPVSDATPDY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLERERLER-LERER-QERE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  787 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two other isoforms, neural Mena+ (see W37153), are also disclosed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%;
21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from a cDNA clone obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 228.5; DB 1;
; Pred. No. 1.8e-06;
84; Mismatches 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PPTSTPPTPPLRHAATRFATSLGSAFHPVLPHY
                                  ----VFHSNTLERKTPI 659
                                                                                                                                                                                                                                                                                                                                                                     PSSPVNTPSSQPPAAKSCAWPTSNF
                                                                                                                                                                                                                                                                                            ---PVLPVCVSSPVPQMPPSP--TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RERLEQLEREQVEWERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ERLEQE - -QLERQRQEREHVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unlike mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse brain
                                                                                                                                                                                                                                                          -- AAAAAPSP
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RESULT R72826 ID R7 AC R7 DT 27 DE HU KW CC KW ir

R72826; 27-FEB-1996

(first

R72826 standard; Protein; 2482

Human mitosin.
Cell cycle; M phase; mitosin;

retinoblastome;

inhibition.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interacts with the retinoblastoma protein (the retinoblastoma tumour suppressor gene product). Mitosin is first synthesised at the G1/S to boundary, it is then phosphorylated from S through M phase, and during comitosis, is closely associated with the centromeres/kinetochores at the comitotic spindle poles. Mitosin is necessary for a eukaryotic cell to conter the M phase of the mitotic cell cycle and its degradation is necessary for a cell to advance on to the next stage. Mitosin is thus cuseful for controlling cell growth as overexpression of mitosin prevents ca cell from exiting the M phase.

CC a cell from exiting the M phase.

CC An anti-mitosin antibody, antibody fragment or a phosphotylated mitosin cell witein ( or nucleic acid encoding it) can also be used to inhibit cell division which is particularly useful for the study of the cell cycle. A further use is to control hyperproliferative cells, and so control cliseases such as psoriasis and breast cancer. It can also be used to block gametogenesis of an immature gamete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR
PR
DR
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PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                           2185
                                                                                                                                                                                                                                                                                                                                              2125
                                                                                                                                                                                                                                                                                                                                                                                                                          2065 AEYQLRLHEAEKKHQALLLDTNKQYEVEIQTYREKLTSKEECLSSQKLEIDLLKSSKEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2006 EL-SGEKNRLAGELOLLLEEIKSSKDOLKELTLENSELKKSLDCMHKDOVEKEGKVREEI 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1948 QDTLEVLQSSYKNLENELELTKMDKMSFVEKVNKMTAKETELQR--EMHEMAQKTAELQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R72829 is human mitosin. Mitosin is involved in the regulation the mammalian mitotic cell cycle. Mitosin as with E2F-1 (see R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       division and/or proliferation
Claim 4; Fig 8B; 61pp; Englis
                                                                                                                                                                                                                                                                                                                                                                                       17]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
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Lee W, Zhu X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-OCT-1994; U12162.
22-OCT-1993; US-141239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Q86851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nhibit its action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 QQMVETLSDENRNLRQELE-----GCYEKVARLQKVETEIQRVSEAYENLVKSSSKRE 78
                                                                                                                        TLHAQIIEKDA----MIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTL
                                                                                     HLCSQQSKQDSRGSPLLGPVVPGPSPIPSVTE-
                                                                                                                                                                                                                                                         S-QLQAAQEKQKTGTVMDTKVDELTTEIKELKETLEEK-
                                                                                                                                                                                                                                                                                              ERELESTRIQORQGNCQPTNVSEYNA---AALMELTREKEERITALEADMTKWEQKYLEEN
                                                                                                                                                                                                                                                                                                                                                                               SNAQAKVVKLEEELKKKQV----YVDKV----EKMQQALVQLQAACEKREQLEHRLRTRL
                                                                                                                                                                                                                                                                                                                                       NNSLKATTQILEELKKTKMDNLKYVNQLKKENERAQGKMKLLIKSCKQLEEEKEILQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALEKAMRNKLEGETRRMHD----
                                       TGSPIMEEKRODKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQ
                                                                                                                                                                                                           VMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TRKTISQLFAKNKESQREKEKLEAELATARSTNED; RRHIEI----RDQAL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 1480. .1659
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                                                                                                                                                                        --SLLISHE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitosin and agents that bind
to promote cell growth or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 226.5; DB 1;
Pred. No. 1e-05;
0; Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --FNRDLRERLETANKQLAEKEYEGSED- 124
PTPATPESFSKKSKKAVMSGIHPAE 2337
                                                                                                                                                                      -KLEKAKEM-
                                                                                   KRLSSGQNKASGKRQRSSGI 2306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 179;
                                                                                                                                                                                                                                                    TKEADEYLDKY 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 it and inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ulation of (see R72824)
                                                                                                                                                                      ---LETQVA 2254
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                                         456
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T such as cancers or psoriasis

SC Claim 1; Column 40-52; 43pp; English.

This is the amino acid sequence for mitosin, a phosphoprotein

C necessary for the cell to ente mitosis. The protein's degradation is

C also necessary for the cell to advance into the next stages of mitosis.

The mitosin protein, can be used to control the growth of cells. An

CC anti-mitosin antibody, a mutant or a non-functional analogue of mitosin

CC can inhibit the mitotic cell cycle by preventing the cells from entering

CC the M phase, and over expression of mitosin or its functional

CC equivalent, would inhibit the cycle by preventing cells from leaving the

CC M phase. Antagonists to this protein can be used to control

CC hyperproliferative cells in, (e.g. thyroid hyperplasia, Grave's disease,

CC psoriasis, benign prostatic hypertrophy, Li-Fraumeni syndrome, breast

CC cancer, sarcomas and other neoplasms, bladder cancer, colon cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTH OK W. P. D. D. C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5710022-A.
20-JAN-1998.
24-OCT-1994;
                                   lung cancer and various leukaemias and lymphomas). Reintroduction or supplementation of lost mitosin function by introduction of the protein or nucleic acid encoding the protein into a cell can restore defective
                                                                                                                                                                                                                                                                                                                                                                                                                          TEXA ) u. Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2429
                                                                                                                                                                                                                                                                                                                                                    New isolated mitosin protein and gene - useful for, e.g. developing products for therapy and diagnosis of hyper-proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; V09076
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-1994; US-328254.
22-OCT-1993; US-141239.
TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia; lymphoma; chromosome segregation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uman mitosin amino acid sequence.
itosin; phosphoprotein; mitotic cell cycle; antibody; analogue;
inhibition; M phase; Antagonist; hyperproliferative cell; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ⊙main
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAPSPATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPVPAPA
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2189
2301
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/note= "optinally A or T"
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/note= "Optionally C or G"
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Best Local Similarity
Matches 139; Conserva
                                                                                                                                                                                                                                                                                                        2429
                                                                                                                                                                                                                                                                                                                                                                 2376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can also cells.
domain
                                                                                                                                                                     Kinetochore protein CENP-F:
Kinetochore protein; CENP-F; cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2125
                                                       domain
                                                                                                                                                                                                  08-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1948 QDTLEVLQSSYKNLENELELTKMDKMSFVEKVNKMTAKETELQR--EMHEMAQKTAELQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                 domain
                                                                                                              domain
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                   R99795
                                                                                                                                                                                                                             R99795 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                       2338 DTEGTE--2---FEPEGLPEVVKKGFADIPTGKTSPYILRRTTM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2185 S-QLQAAQEKQKTGTVMDTKVDELTTEIKELKETLEEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       457
                                                                                                                                                                                                                                                                                                                               575 LVPVPAPAAAQASAPAQTQAPTSAPAVAPTPAPTPTPAVAQAEVPASPATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 QQMVEILSDENRNLRQELE------GCYEKVARLQKVETEIQRVSEAYENLVKSSSKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLHAQIIEKDA----MIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTL
                                                                                                                                                                                                                                                                                                                                                                 ATRTSP-RLAAQKLALSPLSLGKENLAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERGTESNKTAAVAPISVPAPVAAAATAAAITATAATI--TTTMVAAAPVAVAAAAAAPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERELESLRIQOROGNCOPTNVSEYNA -- AALMELLREKEERILALEADMTKWEQKYLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNAQAKVVKLEEELKKKQV----YVDKV----EKMQQALVQLQAACEKREQLEHRLRTRL
                                                                                                                                                                                                                                                                                                        ILREP ---
                                                                                                                                                                                                                                                                                                                                                                                          AAAPSPATAAATAAAVSPAAAGQIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPVPAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPLLSAHSKTGSRDCSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLCSQQSKQDSRGSPLLGPVVPGPSPIPSVTE-----KRLSSGQNKASGKRQRSSGI 2306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNSLKATTQILEELKKTKMDNLKYVNQLKKENERAQGKMKLLIKSCKQLEEEKEILQKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEYQLRLHEAEKKHQALLLDTNKQYEVEIQTYREKLTSKEECLSSQKLEIDLLKSSKEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EL-SGEKNRLAGELOLLLEEIKSSKDQLKELTLENSELKKSLDCMHKDQVEKEGKVREEI 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALEKAMRNKLEGEIRRMHD---
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                                                                                                                                                       antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used for the detection and diagnosis of hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                     -TTKSVPV----NNLPERSPTDSPREGLRVKRGRLVPSPKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEI---RDQAL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
         /label= Globular_domain
/note= "globular domain
repeats of 95 amino acid
                                                                                                                           Location/Qualifiers
                                                                    /label=
                                                                                              /label= Extended_coiled_structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -WENG---3-GG-----PTPATPESFSKKSKKAVMSGIHPAE
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                                                    1610
                                                                                  .1350
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                                                                Extended_coiled_structure
                                                                                                                                                                                                                               3248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 226.5; DE
Pred. No. 1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KLEKAKEM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FNRDLRERLETANKQLAEKEYEGSED-
         main consists acids"
                                                                                                                                                                   cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                        of 2
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                        direct
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Best Local Sim
Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-DEC-1994; US-353700.
(FOXC-) FOX CHASE CANCER CENT.
(UYTE-) UNIV TECHNOLOGIES INT I
Rattner JB, Yen TJ;
WPI: 96-287116/29.
N-PSDB; T34578.
   2578
                                                                    2520
                                                                                                                                                                                              2403
                                                                                                                                                                                                                                                              2343
                                                                                                                                                                                                                                                                                                                           2283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by immunofluorescence microscopy only during the G2 and M phases of a cell cycle. It is the product of a cDNA clone (T34578) isolated from a breast carcinoma cDNA library. Recombinant CENP-F can be produced by expression in prokaryotic or eukaryotic host cells. CENP-F can be used to detect autoimmune antibodies to the protein, which may provide an early diagnosis for the onset of various malignant diseases. Use of CENP-F as a cell cycle marker allows the specific detection of G2 and M phase cells. Sequence 3248 AA;
                                                                                                                          2462 VETLKAKIEGMTQSLRGLELDVVTIRSEKENLTNELQKEQERISELEIINSSFENILQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNA encoding kinetochore protein - used as a marker for the G2 and hases of a cell cycle, partic. for detection of malignant diseases claim 12; Page 41-54; 72pp; English.

A 372 kDa human kinetochore protein, CENP-F (R99795), is detected
                                                                                                                                                                                                                                                                                                                                                                                          `223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9617867-A1.
13-JUN-1996.
08-DEC-1995; U16216.
                                    375
                                                                                                 318
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                                                                                                                                                                 274
                                                                                                                                                                                                                              226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIVSRAQQMVEILSDENRNLRQELEGCYEKVARLQK------VETEIQRVSEAYE
                             PAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDK 409
                                                                                         IQKEEEEILMANKRCLDMEGRIKTLHAQIIEKDAMIKVLQQRSR-KEPSKTEQLSC--MR 374
                                                                                                                                                                                         RARLEADEKKQLCVLQQLKESEHHADLLKGRVENLERELEIARTNQEH-AALEAENSKGE
                                                                                                                                                                                                                                                     EIQIKEESKTAVEMLQNQLKELNEAVAALCGDQEIMKATEQSLDPPIEEEHQLRNSIEKL
                                                                                                                                                                                                                                                                                                                   LKTQIEEMARSLKIFELDLVTLRSEKENLTKQIQEKQGQLSELDKLLSSFKSLLEEKEQA
                                                                                                                                                                                                                                                                                                                                                                                                                 RLETANKQ---LAEK-----EYEGSEDTRKTISQLFAKNKESQR----EKEKLEAELAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               LLVKESESLQARLSESDYEKLNVSKALEAALVEKGEFALRLSSTQEEVHQLRRGIEKLRV 2222
                                                                                                                                                             QKYLEENV-----MRHFALDAAA---
                                                                                                                                                                                                                       LESLRIQORQGNC--QPTNVSEYNAAAL-----
                                                                                                                                                                                                                                                                                           LVQLQ---
                                                                                                                                                                                                                                                                                                                                                    ARSTNEDQRRHIEIRDQALSNAQAKVVKLEEELKKKQVYVDKVEKM-
                                                                                                                                                                                                                                                                                                                                                                                  RIEADEKKQLHIAEKLKERERENDSLKDKVENLERELQMSEENQELVILDAENSKAEVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLVKSSSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEVKEKTELLQTLSSDVSELLKDKTHLQEKLQSLEKDSQALSLTKCELENQIAQLNKEKE
                                                             -EKEQEKVQMKEKSSTAME-MLQTQLKELNERVAALHNDQEACKAKEQNLSSQVECLELE 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "the C-terminal domain is predicted form a proline-rich (10.6%) highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (pI 10) globular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -REALEKAMRNKLEGEIR----RMHDFNR---DLRE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 225; DB 1;
Pred. No. 1.8e-05;
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                                                                                                                                                                                                                                                                                          -AACEKRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                        --TVAAQRDTTVISHSP--NTSYDTALEAR 317
2610
                                                                                                                                                                                                                       -MELLREKEERILALEADMIKWE 273
                                                                                                                                                                                                                                                                                      -----QLEHRLRTRLERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 71
                                                                                                                                                            SMOOTH EUSCLE; myosin heavy chain; SMI isororm; raburc, c., gene therapy; mouse; SM2 isoform; retrovirus; adenovirus; gene therapy; mouse; SM2 isoform; artery catheterisation; sometherapy and adenovirus; coronary artery catheterisation; sometherapy and s
                                                                                                                                     Mus musculus.
WO9623069-A1.
                                                                                                                                                                                                          25-MAR-199/ (ILISE EHLI)
Smooth Edscle myosin heavy chain SMI isoform; rabbit; arteriosclerosis;
                           (YESS-)
                                              (OSAP ) OSAKA PREFECTURAL GOVERNMENT
                                                                       25-JI.N-1995;
                                                                                         25-JAN-1996;
                                                                                                              01-AUG-1996.
                                                                                                                                                                                                                                                                    25-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                               W00024 standard;
W00024;
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Trypanosoma cruzi Tulahean strain C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W26540 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 ААРРАКАААРРАКТААРРАКТААРРАКАААРРАКАААРРАКАААР-РАКААААРАКАААА 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 APVAAAATAAAITATAATITTTMYAAAPVAVAAAAAPÄÄÄAAAPSPATAAATAAAVSPAAA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton RL
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14-NOV-1995; US-557309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; critope; vaccine; protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 AAAAAKQKAAAKKAAAPSGKKSAKAAAP- AKAAAAPAKAAAPPAKTAAAPAKAAAPAKA 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAQTQAPTSAPAVAPTPAPTPTPAVAQAEVPASPATGP
                                                                                                                                                                                                                                                                                                                                                                                                                            PAKAAAPPAKAAAPPAKAAAP-FAKAAAP-PAKA JAAP
VESSEL RES LAB CO
E, Hasegawa K, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                     J00134.
JP-010085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                  Protein; 1972 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 AA
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Pred. No. 5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunity; Chagas disease;
                                                                                                                                                                                                                                                                                                                                                                                                                              433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                 restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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sugawara M, Takahashi K; wel, 96-362693/36.

araknya E,

Ishiyama H,

Matsuda

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RESULT
W06913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ?יירץ Match
                                                                                                                                                                                                                                                            W06913 standard; Protein; W06913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1776
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                                                                                        region
                                                                                                                                                                                                                                                                                                                                                                                                               1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1614 LAAAAKKKLEGDLKDLELQADSAIKGREEAIKQLRKLQAQMKDFQRELDDARASRDEIFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1554 DVQATEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQLHEYETELEDERKQRA 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the smooth muscle myosin heavy chain SM1 isofo protein. The SM1 coding sequence was isolated from a mouse embryo cDNA library using probes based on the rabbit smooth muscle myosin heavy cha SM2 isoform. The isolated coding sequence is included in the gene therapy vector of the invention consists
14-MAR-1995; US-403379
               26-SEP-1996.
12-MAR-1996;
                                            WO9629605-A2
                                                                                                                                                  region
                                                                                                                                                                               Trypanosoma
                                                                                                                                                                                             leishmaniasis.
                                                                                                                                                                                                           L19E homologue;
                                                                                                                                                                                                                                            02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1674 TSKENEKKAKSLEADLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNTLQDEKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adenovirus or animal-expression plasmid vector (such as pCXN2 or PAGE208). The vector can be used in the gene therapy treatment of arteriosclerosis, particularly for the reduction of restenosis occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arteries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy vector of the invention. The vector of the invention consists the coding sequence inserted into a retrovirus, adenovirus, associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a vector for gene therapy for recoronary artery catheterisation Claim 5; Page 14-27; 42pp; Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      following coronary
                                                                                                                                                                                                                                                                                                                                                     347
                                                                                                                                                                                                                                                                                                                                                                            335 MEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 LERELESLRIQQRQGNCQPTNVSEYNAAALMELLREKEERILALEADMIKWEQKYLEENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                            282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 21.7 es 86; Conservative
                                                                                                                                                                                                                          cruzi L19E homologue TcE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding smooth muscle myosin heavy chain SM1 isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNKESQR---
                                                                                                                                                                                                                                                                                                                                              KDKKLKEVLLQVEDERKMAEQYKEQAEKGNTKVKQL 1882
                                                                                                                                                                                                                                                                                                                                                                                                              LRSKLQEVEGAVKAKLKSTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                       MRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EILSDENRNLR-----QELEGCYEKVARLQKVETE----IQRVSEAYENLVKSSSKREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEIRDQALSNAQAKVVKLEEELKKKQVYVDKV-EKMQQALVQLQAACEKREQLEHRLRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAE-----KEYEGS-EDTRKTISQLFA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T34291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1972 AA;
                                                                                                                                                             cruzi strain MHOM/CH/00/Tulahuen
Location/Qualifiers
              U03380
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                             TCE;
                                                                                                                 are useful
                                                                                                     cruzi and Leishmania
                                                                                                                               /note= "polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ARIAQLEEELEEEQGNMEAMSDRVRKATLQ-----AEQLSNELAT-
                                                       tandemly arrayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        artery catheterisation
                                                                                                                                                                                                          diagnosis; infection; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%;
21.7%;
                                                    "amino acids 137-247 comprise 16 copies amly arrayed 7-amino acid repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAQKNESARQQLERQNKE---
                                                                                                                                                                                                                                                                       262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 213; DB 1; Pred. No. 5.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reduction
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                                                                                                                                                                                                                                                                                                                                                                                                         -AALEAKIAQLEEQVEQEAREKQAATKSLKQ 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EKEKLEAELATA---RSTNEDQRRH 162
                                                                                                                   comprising s for screer
                                                                                                     infection'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of re-stenosis following
                                                                                                                 screeninf
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                                                                                                                 amino acids 1–143 ninf for T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122;
                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain
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RESULT
W89253
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                         27-APR 1998; U08439
23-OCT 1997; US-063595.
28-APR-1997; US-044428.
20-MAY-1997; US-047222.
11-JUN-1997; US-049477.
11-JUN-1997; US-049756.
18-JUN-1997; US-049914.
                         The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents human ALF. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists,
     or prevent diseases associated with abnormal
                                                                                                           New nucleic acid encoding specific protein useful for identifying specific modulators prevention of cancer and neurodegenerative Claim 2; Page 160-164; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCE amino acid sequence was deduced from a cDNA clone (746148) isolated from an amastigote library. Epitopes such as TCET (W06914) derived from the TCE repeat region can be used in method: for detecting T. cruzi infection (Chagas' disease) and in vaccine compsns. Polypeptides comprising the L19E homologous region can used in methods for detecting Leishmania or T. cruzi infection.
                                                                                                                                                                                                            App H, Clary D, Courtneidge (Markby D, Onrust S, Peles E,
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens, WO9849317-A2:
                                                                                                                                                                                 N-PSDB; V81748
                                                                                                                                                                                                                                            (SUGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          type I receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W89253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W89253 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting and or antibodies
                ncluding NBP) in vivo or in vitro.
                                                                                                                                                                                                                                                                                                                                                                           35-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disease; neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal portion to the eukaryotic ribosomal protein L19E. T
C-terminal portion comprises a 7-amino acid repeat region. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 2; 59pp; En
The 35 kDa T. cruzi TcE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 ААААРАКААЛАРАКААТАРАКААААРАКТА-ААРАКАААРАКА-АЛАРАКА-АТАРАКАА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 AAAATAAAITATAATITTTMVAAAP---VAVAAAAAAPA-AAAAAPSPATAAATAAAVSPAA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 AGQIPAAASVASA-AAVAPSAAAAAAVQVAPAAPAPVPAPALVPVPAPAAAQASAPAQTQ 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 AAAAAAKOKAAAKK-----AAAPSGKKSAKAAIAPAKAAAAPAKAAAAPAKAAAAPAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 APTSAPAVAPTPAPTPTPAVAQAEVPASPATGP
                                                                                                                                                                                             99-009434/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAPAKAATAPAKAAT-APAKA-AAAPAKAATAP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96-485445/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTP05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTP10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing T. cruzi infection - contg. or reactive with antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                   rriu; SAD; ALP; ALK-7; protein tyrosine phos
serine/threonine kinase; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                       Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen (W06913) shows homology in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1274
                                                                                                                                                                                                              SA, Hui T
E, Plowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 213; DB 1;
Pred. No. 3.9e-06;
                                                                                                                                                                                                              Hui TH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        disease.
These substances are used to abnormal signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                    survival; Alzheimer's
                                                                                                                                                                                                                             Jallal
                                                                                                                               disease
                                                                                                                                              tyrosine phosphatases for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            using polypeptide(s) epitope(s) of T. cru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphatase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in methods
                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
                          ed to identify antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its
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               treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ទននន្តន្តន្តន្តន្តន
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathways that involve the proteins, particularly cancer (e.g. leuka and lymphoma), while modulators of ALK-7 (which is a type I receptc serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's
                                                                                                                                                                                                                                                                                                                                           442 LSAHSKTGSRDCSTQTERGTESNKTAAVAPISVPAPVA--AAATAAAITATAATITTTMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly for treating Alzheimer's, Parkinson's or Huntington diseases. Nucleic acid fragments of the polynucleotides encoding
    642
                                      661
                                                                                                                                                         533
                                                                                                                                                                                                                                                                          500
                                                                                                                                                                                                                                                                                                                                                                                             376
                                                                                                                                                                                                                                                                                                                                                                                                                     382 ISNAGSGLLSHSSTLTGSPIMEEKRDDKSWKGSLGILLGGDYRAEYVPSTPSPVPPSTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 RIQORQGNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQ--KYLEENVMRHFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 VGQAGAISITSKAELAEVRREWAKYMEVHEKASFTNSELHRAMNLHVGNLRLLSGPLDQV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 CAALSVRPDTVRNLVQSMQVLSGVFTDVEASLKDIRDLLE--EDELLEQKFQ-----EA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 AQQMVEILSDENRNLRQELEGCYE-KVARLQKVETEIQRVSEAYENL-VKSSSKREALEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AHEASSLYSEEKAKLLREMMAKIEDKNEVLDQFMDSMQLDPETVDNLDAYSHIPPQLMEK
PGVLGQPP
                        --ILGQEP 666
                                                                                                                                                                                                                          PRSSPQHGVVSSPYVGVGPAPPVAGLPSAPPPQFSGPELAMAVRPATTTVDSIQAPIPSH
                                                                                                                                                                                                                                                                AAAPVAVAAAAAPAAAAAPSPATAAATAAAVSPAAAGQI-----PAAASVASAAAVAPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAAAT-----VAAQRDTTVISHSPNTSYDT-----ALEARIQKEEEEILMANKRCLDM
                                                                    PQPHPQPHPSQAFGPQPPQQ---PLPLQHPHLF--PPQAPG
                                                                                                         PAPTPTPAVAQAEVPASPATGPGPHRLSIPSLTCNPDKTDGPVFHSNTLERKTPIQ----
                                                                                                                                             TAPRPNPTPAPPPPCFPVPPPQPLPTPYTYPAGAKQPIPAQHHFSSGIPTGFPAPRIGPQ
                                                                                                                                                                                 AA----AAAVQVAPAAPAPVPAPALVPVPAPAAAQASAPAQ----TQAPTS--APAVAPT
                                                                                                                                                                                                                                                                                                      -----GPGPHYLSGPLPPGTYSGPTQLIQP-RAPGPHAMPVAPGPALYPAPAYTPELGLV
                                                                                                                                                                                                                                                                                                                                                                                     AGDPPEELRSLPPDMVAGPRLPD----TFLGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESKVAALLERTQSTCQAREAARQQLLDRE-----LKKKPPPRPTAPKPLLPRREESEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCALTEANVQYAAVRRVLSDLDQKWNSTLQTLVASYEAYEDLMKKSQE----GRDFYADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSNAQAKVVKLEEELKKKQVYVDKVEKMQQALVQLQAACEKREQLEHRLRTRLERELESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISQLFAKNKESQREKEKLEAELA-----TARSTNEDQRRHIEIR------DQA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------AMRN-----KLEGEIRRMHDENRDLRERLETANKQLAEKEYEGSEDTRKT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 212.5; DB : 20.7%; Pred. No. 3.1e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DITASLYTTDHSEMKKL-FEEQLKKYDQLKVYLEQNLAAQDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VLQNLKRILAKVQEMRDQRVSLEQQLRELIQKD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -HAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306;
                                                                                                                                                                                                                                                                                                                                                                                 ---ATPLHFPPSPFPSST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                    LLPPQSPYPYAPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1274;
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RESULT W02258

RB

W02258 standard; Protein; 1411 AA. W02258;

W76734 :tandard; Protein; W76734: 15-JAN-1969 (first entry)

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(first entry)

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Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transformed cells can be collured to produce the antigen p162, for in exact (differential) diagnosis of rheumatic disease, i.e. they can detect, in immunoassays, Western blots, etc., rheumatism-specific auto-antibodies. The antigen can be used therapeutically, in the removal of auto-antibodies from the circulation, or when coupled to a cytotoxin, the elimination of auto-antibody-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding nucleolar endosomal auto-antigen diagnosis of rheumatic disease, in gene therap specific auto-antibodies Claim 1; Fig 2; 15pp; German.
   793
                                                               733
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                                                                                                                                                                                                                                                                                                                                                                 436 KLKEQRQLSSEK---LMDKEQQVADLQLKLSRLEEQLKEKVTNSTELQHQLDKTKQQHQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Auto-antibody; p162; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleolar/endosomal auto-antigen p162.
Auto-antibody; p162; rheumatic disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1997 (first entry)
                               377 KSLMST 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; T58751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Renz M, Seelig HP;
WPI; 96-403153/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        148
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                                                                                                                                                                                                                                                                                                                                                                                                                                    382 SEVETKYOH---
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                                                                                                                                                                                                                                                                                                     QQALQQSTTAKLREAQNDLEQVLRQIGDKDQKIQNLEALLQKSKENISLLEKEREDLYAK
EALES: 798
                                                                                                                                                                               QDRVLSLETSVNELNSQLNESKEKVSQLDIQIKAKTELLLSAEAAKTAQRADLQNHLDTA
                                                                                                                                                                                                                                        IQAGEGETAVLNQLQEKNHTLQEQVTQLTEKLKNQSESHKQAQENLHDQVQEQKAHLRAA
                                                                                                                                                                                                                                                                                                                                                                                                ELATARSTNEDQRRHIEIRDQALSNAQAKVVKLEEELKKK-----QVYVDKVEKM---
                                                         KKLEA(:SLEVKASKEQALQDLQQQRQLNTDLELRATELSKQLEMEKEIVSSTRLDLQKKS
                                                                                          KTLHAQ: IE--
                                                                                                                    QNALQDKGQELNKITTQLDQVTAKLQDKQEHCSQLESHLKEYKEKYLSLEQKTEELEGQI
                                                                                                                                                                                                                                                                               IQQRQGNC--
                                                                                                                                                                                                                                                                                                                                          QQALVQLQAA -- CEKREQLEHRLR --
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRKTISQLFAKNKESQREKEKLEA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESYSKKNIQATLHQKDLDCQQLQSRLSASETSLHRIH-----VELSEKGEATQKLKEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EILSDEN--RNLRQELEGCYEKVARLQKVSTEIQRVSEAYENLVKSSSKREALEKAMRNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .ymphocytes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                          -KDAMIKVLQQRSR
                                                                                                                                                                                                                                                                                                                                                                                                                              -LKAEFKQLQQQREEKEQHGLQ-LQSEINQLHSKLLETERQLGEAHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 211; DB 1; 22.2%; Pred. No. 4.4e-05; tive 75; Mismatches 155;
                                                                                                                                                 DTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDMEGRI
                                                                                                                                                                                                                                                                       ---QPT-----LREK 258
                                                                                                                                                                                                               KWEQKYLEENVMRHFALDAAATVAAQR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for exact and for removal
                                                                                                                                                                                                                                                                                                                                   ---TRLERELESL--R
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17;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mechanisms of respiratory tract disease
Claim 2a; Page 28-31; 54pp; Japanese.
This sequence represents a human Rho target protein, mDia (mammalian diaphanous). This protein has active type Rho protein-combining ability, has proline-combining ability, has a M.W. of 150 KDa measured by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and its gene is positioned at human chromosome 5q31.2. The nucleic acid can be used for the recombinant production of the protein. The protein is useful for the elucidation of mechanism of diseases such as respiratory tract oversensitiveness, bronchial asthma, acute marrow leukaemia and marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rho Protein; mDia; mammalian diaphanous; target protein; human; Rho protein-combining; proline-combining; chromosome 5q31.2; disease; respiratory tract; oversensitiveness; bronchial asthma; marrow leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Rho target protein and its gene - useful for elucidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; V62933
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25-MAR-1997; JP-090170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marrow dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mDia Rho targeting protein
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463 SNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAAAPA-----AAAA
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                                                                                                                                                                                                                                                                                                                                                             QVLQDLREIENEDMRVQLNVFDEQGEEDSYDLKGRLDDIRMEMDDFNEVFQILLNTVKDS
                                          LEDAKKEMASLSAA - - -
                                                                           KRDDKSWKGSLGILLGGDYRAEYVPSTPS--PVPPSTPLLSAHSKTGSRDCSTQTERGTE 462
                                                                                                                                                                                                                                                                                  KAEPHFLSILQHLLLVRNDYEARPQYYKLIEECISQIVLHKNGADPDFKCRHLQIEIEGL
                                                                                                                                                                                                                                                                                                                                                                                                        -----RELES--LRIQ----QRQGNCQP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QVYVDKVEKMQQAL-----VQLQAAC-----EKREQLEHRLRTRLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IKTMLETEEGILLLVRAMDPAVPNNMIDAAKLLSALCILPQPEDMNERVLEAMT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSKAGMSQKESSKSAMMYIQELRSGLRDMPLLSCLESLRVSLNNNPVSWVQTFGAEGLAS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSASYGDDPTAQSLQDVSDEQVLVLFEQMLLDMNLNEEKQQPLREKDIIIKREMVSQYLY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSASYQPVP-ADPFAIVSRAQQMV:--EILSDENRN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163;
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                                                                                                                        -EKDAL-----HSEKQQIATEK
                                                                                                                                                       IEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSHSSTLTG--SPIMEE 404
                                                                                                                                                                                                 IDQMIDKTKVEKSEAKAAELEKKLDSELTARHELQVEMKKMES----DFEQKLQDLQG--
                                                                                                                                                                                                                                       VAAQRDTTVISHSP-----NTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTLHAQI 346
                                                                                                                                                                                                                                                                                                                                                                                                                                              ERAEMDEVERFOPLLDGLKSGTTIALKVGCLQLINALITPAEELDFRVHIRSELMRLGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLDILKRLHD-----EKEETA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRK----TISQLFAKNKESQREK 142
                                                                                                                                                                                                                                                                                                                          ----ERILALEADMTKWEQKY--LEENV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%;
                                        ---AITVPPSVPSRAPVPPAPPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 209.5; DB 1;
Pred. No. 5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      --TNVSEYNAA--ALMELLREK 258
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                                                                                                                 -QDLEAEVSQLTGEVAKLTKE
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                                     ----PGDSGT- 638
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                      Streptococcus uberis su-1.4 Its amino acid sequence was deduced from the novel isolated lbp gene (see v42601). The LBP is luctoferrin species-specific; human lactoferrin does not effectively block binding of bovine lactoferrin. The invention provides recombinant vectors, transformed host cells and methods producing recombinant bovine LBP of S. uberis. The bovine LBP producing recombinant bovine LBP of S. uberis. The bovine LBP immunogenic fragments and/or chimeric proteins can be used, either alone or in combination with other antigens, in novel subunit vaccines for the prevention and treatment of S. uberis infections particularly mastitis, as well as in diagnostic methods for
            determining
                                                                                                                                                                                               Claim 2; Fig 2A-C; 105pp; English.
This is the bovine lactoferrin binding protein (LBP) of
                                                                                                                                                                                                                                                                                                                  (UYSA-) UNIV SASKATCHEWAN.
Jiang M, Maclachlan PR, Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                        WO9821231-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W63043 standard; Protein; 561 AA
                                                                                                                                                                                                                                               Immunogenic Streptococcus uberis protein(s) that bind bovine actiferrin associated regulatory protein, useful in vacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus uberis
                                                                                                                                                                                                                                    reatment and prevention of mastitis
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14-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 PSPATAAATAAAVSPAAAG-QIPAAASVASAAAVAPSAAAAAAVQVAPAAPAPVPAPA-L 575
                                                                                                                                                                                                                                                                                       -PSDB; V42601
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us uberis bovine lactoferrin binding protein.
              the presence of S. uberis infections
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US-031117.
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/note= "alternative
Met-11"
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Best Local Similarity
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WPI; 98-230690/20.
N-PSDB; V21518.
Transgenic mouse models for congestive heart failure and hypertrophic cardio-myopathy - used to study molecular and
                                                                         02-APR-1998.
26-SEP-1997; U17296.
26-SEP-1996; US-026742.
(LEIN/) LEINWAND LA.
                                                                                                                                                                                                                                                                                                 dilated or hypertrophic cardiomyopathy; acute aortic regurgitation; tricuspid stenosis; constrictive pericarditis; hypertension;
                                                                                                                                  WO9813476-A1.
                                                                                                                                                                                                                               Rattus norvegicus.
                                                                                                                                                                                                                                               hyperthyroidism; anaemia; arteriovenous
Paget's disease; transgene.
                                                                                                                                                                                                                                                                        acute infective endocarditis; ischaemic heart disease; primary myocardial disease; valvular disease; pericard
                                                                                                                                                                                                                                                                                                                           Actin binding domain; alpha myosin heavy chain; bridging; mouse; transgenic mammal; congestive heart failure; study; treatment; diet; exercise; effects; identification; hypertrophic cardio-myopathy.
                                                             Vikstrom KL
                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                             Actin binding domain; alpha
                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus mutant
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                                                                                                                                                                                        Region
                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                           /note= "Arg403Gln
468. .475
                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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                                                                                                                                              "nonmyosin
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Best Local Similarity
                                                                                                                             1412
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diet rtc:
                       921731;
                                      W21731 standard; Protein;
                                                                                                                                                                                                                                                                        1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heart disease; hypertension; primary myocardial disease; valvular or pericardial disease; hyperthyroidism; anaemia; arteriovenous fistula; beri-beri and Paget's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiomyopathy; acute aortic regurgitation; tricuspid sto-
constrictive pericarditis; acute infective endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specifically mice. They can be used as a model for studying congestive heart failure (CHF) or hypertrophic cardiomyopathy. Such animals are used to study molecular and cellular events associated with CHF; to identify compounds for treating CHF, and in evaluating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Pages 53-58; 75pp; English.
The sequence is that of a mutant rat alpha-myosin which was used in the development of transgenic manual forms.
       01-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     effects of diet and exercise on CHF. Conditions associated that can be evaluated this way are dilated or hypertrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                              365
                                                                                                                                                                                                                                   324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    997 LERAKR-KLEGDLKLTQESIMDLENDKLQLEEKLKKKEFDISQQNSKIEDEQALALQLQK 1055
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                                                                                                                          SOSELESSOKEARSLSTELFKLKNAYEESLEHLETF - - -
                                                                                                                                                         SKTEQLSCMRPAKS----LMSISNAGSGLLSHSSTLTGSPIMEEKRDDKS
                                                                                                                                                                                        AVEAVNAKCSSLEKTKHRLQNETEDLMYDVERSNAAAAALDKKQRNFDKTLAEWKQKYEE
                                                                                                                                                                                                                                                               QYEEEMEAKAELQR----VLSKANSFVAQWRTKYETDAIQRTEELEEAKKKLAQRLQDAEE
                                                                                                                                                                                                                                                                                                                                                                                                      ELDDVTSHMEQIIKAKANLEKVSRTLEDQANEYRVKLEEAQRSLNDFTTQRAKLQTENGE 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REAEFOKMRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKQVYVUKVEKMQQALVQLQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLKENQARIEELEEELEAERTARAKVEKLRSDLTRELEEISERLEEAGGATSVQIEMNKK 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIAKLTKEKKALQEAHQQALDDLQAEEDKVNTLTKSKVKLEQQVDDLEGSLEQEKKVRMD 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVSRAQQMVEILSDENRNLRQELEGCYEKVARLQKVETEI-QRVSEAYENLVKSSSKREA 79
                                                                                                                                                                                                                              EILMANKRCLDME-----GRIKTLHAQIIEKDAMIKVLQQRSRK--
                                                                                                                                                                                                                                                                                                                                  LARQLEEKEALIWOLTRGKLSYTQQMEDLKRQLEEEGKAKNALAH-ALQSARHDCDLLRE
                                                                                                                                                                                                                                                                                                                                                                         LMELLREKEERILALEADMTKWEQ-----KYLEZ----
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q-----QRQGNCQPTN----VSEYNA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNKESQREKEKLEAEL---ATARSTNE----DQRRHIEIRDQALSNA-QAKVVKLEEELK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAEKEYEGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116;
                                                                                                                                                                                                                                                                                                   --- ATVAAQRDTTVISHSFN----TSYDT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.18;
                                        2272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ACEKREQLEH--RLRTRLERELESLRI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conditions associated with CHF
                                                                                                                                                                                                                                                                                                                                                                         -NVMRHFALDAA--
                                                                                                                                                                                                                                                                                                   -----ALEARIQKEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stenosis;
                                                                                                                        1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1886;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AA 250
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RESTLT 1.5
W21731
ID W21731
AC 921731
DT 11-CT
DE GAL4H
KW NIP-1;
KW NIP-1;
KW malign
GS HOMO S
FH Key
FT domain
                                                    GAL4/HANUMA fusion protein.
NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein;
                                           Homo sapiens
Location/Qualifiers
1. .147
/Tabel= GAL4_DNA_binding_domain
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Best Local Similarity 21.2
Matches 101; Conservative
1564 ----GELIPLRQKVAEQE---RTAQQLRAEKASYAEQLSMLKKAHGLLAEENRGLG 1612
                                                                                                                                                                     1452
                                                                                                                                                                                                                                                    1392
                                                                                                                                                                                                                                                                                                                                                                                                   1272 TEPTGPKLEALRAEVSKLEQQCQKQQEQADSLERSLEAERASRAERDSALETLQGQLEEK 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1156 RGQQEREVARLTQERGRAQADLALEKAAR---AELEMRLQNALNEQRVEFATLQEALAHA 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with a known NIP are used to modulate cell division and/or proliferation Ab, raised conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in W21731-32 represent fusion proteins which con NuMA (nuclear mitotic apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA
                                                                                                                                                                                                                                                                                                                      1332 AQELGHSQSALASAQRELAAFRTKVQDHSKAEDEWKAQVARGRQEAERKNSLISSLEEEV 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1213 LTEK-EGKDQELAKLRGLEAAQIKELEELRQTVKQLKEQLAKKEKEHASGSGAQSEAAGR 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (which can also be detected by nucleic acid sequencing). malignancy is related to defects in NumA or NIP, it can administration of the appropriate functional protein.
                                                   333
                                                                                                                                                                                                                                                                                           197
                                                                                                                                                                                                                                                                                                                                                                        160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which may be markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 28-36; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding nuclear mitotic appts. interacting proteins - useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McPherson SMG, Sn
WPI; 97-077270/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 MRNKLEG---EIRRMHDFN------RDLRERLETANKQLAEKEYE----GS------ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PSDB; T77782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 RAQQMVEILSDENRNLRQELEGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREALEKA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis
                                       LDMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSG
                                                                                                                    ALDAAATVAAQRDTTVISH-`SPNTSYDTALEARIQKEEE-----EILMANKRC 332
                                                                                                                                                                                                  ESLRIQQRQGNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQKYLE-ENVMRHF 285
                                                                                                                                                                                                                                          SILNROVLEKEGESKELKRLVMAESEKSOKLEERLRLLOAETASNSARAAERSSALREEV
                                                                                QLEHTSTQALVSELLPAKHLCQQLQAEQAAAEKRHREELEQSKQAAGGLRAELLRAQREL 1563
                                                                                                                                                             QSLREEAEKQRVASEN-----LRQELTSQAERAEELGQELKAWQEKFFQKEQALSTL 150:
                                                                                                                                                                                                                                                                                     ---MQQALVQ-----LQAAÇEKREQLEHRLR----
                                                                                                                                                                                                                                                                                                                                                                      RRHIEIRDQALSNAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EDTRKTISQLFAKNKESQREKEKLEAELATARSTN----
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/label=_Residues_18-2116_of_NuMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148. .174
/label=_Hemaglutinin_epitope
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/label= Coiled_coil_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for aberrant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 204; DB 1;
Pred. No. 0.00022;
2; Mismatches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (including malignant) cell growth leic acid sequencing). Also where
                                                                                                                                                                                                                                                                                                                                                                ----AKVVKLEEELKKKQVYVDKVEK-- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 130;
                                                                                                                                                                                                                                                                               -----TRLEREL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EDQ 159
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                                                                                                                                                                                                                                            1451
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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

Run

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Result
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3347
1 MPRAQPSSASYQPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130275 seqs,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pass the threshold: 130275
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS9_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS9_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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                                                                                                                                                     2101
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US-08-282-845-2

PCT-US94-00324-1

PCT-US93-03077-1

US-08-450-360-2

US-08-056-200-94
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US-09-080-897-4
US-08-685-576-1
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US-08-470-950-4
US-08-467-781-4
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US-08-685-576-4
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US-09-080-897-2
US-08-195-487-4
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                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                         Rest Local :
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                                                                    2006 EL-SGEKNRLAGELOLLLEEIKSSKDOLKELTLENSELKKSLDCMHKDOVEKEGKVREEI 2064
                                                                                                                                                                 1948 QDTLEVLQSSYKNLENELELTKMDKMSFVEKVNKMTAKETELQR--EMHEMAQKTAELQE 2005
                                                                                                                                                                                                           26 QQMVEILSDENRNLRGELE-----GCYEKVARLQKVETEIQRVSEAYENLVKSSSKRE 78
                                                                                                                     79 ALEKAMPNKLEGEIRRMHD-----
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	Sequence 6, Appli	Sequence 4, Appli	Sequence 4, Appli		Sequence 62, Appl	·	Sequence 2, Appli	Sequence 2, Appli	2,	Sequence 4, Appli

ALIGNMENTS

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MOLECULE TYPE: protein 1:5-08-328-254-6
                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141
FILING DATE: 22-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
PEGISTRATION NUMBER: 31,815
                                                                                                          TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
TERORMATION FOR SEQ ID NO: 6:
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                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2482 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
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                                                                                                                                                TELLECOMMUNICATION INFORMATION: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/328,254 FILING DATE: 24-OCT-1994
                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P-CJ
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Diego
                                                     amino acid
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                                                                          2482 amino acids
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6.8%;

%; Score 226.5; DB 1; %; Pred. No. 6.1e-07; 100; Mismatches 233;

Indels 179; Length

Gaps

26;

2482;

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Db 2065 AEYOLALHARAEKKHOALLLDTNKOYEVETOTYREKLTSKEECLSSOKLEIDLLKSSKEEL 2124 Oy 171 SHAAAKWYLEELKKKOYYYDVYERMQOALVOLAACEKREOLEHRILTRI 222 181 SHASLKATTQILEELKKTKMONLKYNQLKKENEBAGGKMKLLIKSCKOLEEKEILAKEL 2184 Oy 223 ERELESIRKOORGOKOOFTWOTKYDELTEIKLEKTHOOLEKYNGLKEEREILALEADHTKKEGKILEEN 200 185 S-OLGAAQEKOKTOTYNOTKYDELTTEIKLEKTHOOLEKYNGKEETLIAAKKCLAUKGKILEEN 200 185 S-OLGAAQEKOKTOTYNOTKYDELTTEIKLEKTHOOLEKYNGKEETLIAAKKCLAUKGKILEEN 200 223 C

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MOLECULE TYPE: PI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
US-08-353-700-1
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PCT-US95-16216-1
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    COUNTRY: USA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERAT
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GENERAL INFORMATION:
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SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2223 RIEADEKKOLHIAEKLKERERENDSLKDKVENLERELOMSEENQELVILDAENSKAEVET 2282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 PAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDK 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 ARSTNEDQKRHIEIRDQALSNAQAKVVKLEEELKKKQVYVDKVEKM------QQA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 LVQLQ----
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                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Rattner, Jerome B.
TILE OF INVENTION: Nucleic Acid Encoding a Transiently
TILE OF INVENTION: Expressed Kinetochore Protein, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 NLVKSSSK------REALEKAMRNKLEGETR-----RMHDFNR---DLRE 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application PC/TUS9516216
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                                                                                           Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QLEHRLRTRLERE 225
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PRIOR APPLICATION

09-DEC-1995

US 08/353,700

FILING DATE: CLASSIFICATION:

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                                                                                                                                                                                              RESULT
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                                                                                                                   Sequence 1, Application US/08403379A Patent No. 5756662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                    2578
                                                                                                                                                                                                                                                                                                                                                 2520 - EKEQEKVQMKEKSSTAME-MLQTQLKELNERVAALHNDQEACKAKEQNLSSQVECLELE 2577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                2462 VETLKAKIEGMTQSLRGLELDVVTIRSEKENLTNELQKEQERISELEIINSSFENILQ-- 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2343 EIQIKEESKTAVEMLQNQLKELNEAVAALCGDQEIMKATEQSLDPPIEEEHQLRNSIEKL 2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2403 RARLEADEKKQLCVLQQLKESEHHADLLKGRVENLERELEIARTNQEH-AALEAENSKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2283 LKTQIEEMARSLKIFELDLVTLRSEKENLTKQIQEKQGQLSELDKLLSSFKSLLEEKEQA 2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2223 RIEADEKKQLHIAEKLKERERENDSLKDKVENLERELQMSEENQELVILDAENSKAEVET 2282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2163. LLVKESESLQARLSESDYEKLNVSKALEAALVEKGEFALRLSSTQEEVHQLRRGIEKLRV 2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2103 AEVKEKTELLQTLSSDVSELLKDKTHLQEKLQSLEKDSQALSLTKCELENQIAQLNKEKE 2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 QKYLEENV-----MRHFALDAAA-----TVAAQRDTTVISHSP--NTSYDTALEAR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       375 PAKSLMSISNAGSGLLSHSSTLTGSPIMEEKRDDK 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 LESLRIQORQGNC--QPTNVSEYNAAAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 ARSTNEDQRRHIEIRDQALSNAQAKVVKLEEELKKKQVYVDKVEKM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 RLETANKQ----LAEK------EYEGSEDTRKTISQLFAKNKESQR----EKEKLEAELAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTI-SENSE:
                    TLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 09-DE
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                                                                                                                                                                                                                                                               KAQLLQGLDEAKNNYIVLQSSVKG--LIQEVEDGK 2610
                                                                                                                                                                                                                                                                                                                                                                                                 IQKEEEEILMANKRCLDMEGRIKTLHAQTIEKDAMIKVLQQRSR-KEPSKTEQLSC--MR 374
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                                                                      Reed, Steven G.
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COMPOUNDS AND METHODS FOR THE DETECTION OF T. CRUZI INFECTION 9
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ZIP: 98104-7092 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,

APPLICATION, DATA

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Best Local S
Matches 74
                                                                                                                                                                                                                                                 Sequence 51,
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                               535 AGQIPAAASVASA-AAVAPSAAAAAAVQVAPAAPAPVPAPALVPVPAPAAAQASAPAQTQ 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                              166 АЛААРАКАЛААРАКАЛТАРАКАЛААРАКТА-ААРАКАЛАРАКА-АЛАРАКА-АТАРАКАА 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 PASAAAKQKAAAKK-----AAAPSGKKSAKAAIAPAKAAAAPAKAAAAPAKAAAAPAK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 AAAATAAATTATAAATTTTTMVAAAP----VAVAAAAAAPA-AAAAAPSPATAAATAAAVSPAA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 223 PAPAKAATAPAKAAT-APAKA-AAAPAKAATAP 253
                                                                                                                                                                                                                                                                                                                                                               594 AFTSAPAVAPTPAPTPTPAVAQAEVPASPATGP 626
ZIP: 981
                                        STREET: 6300 CCITY: Seattle
                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 14-MA
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                              OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /AGENI ANTINHER: 31,392
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                          Washington
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                                                                                                                                                                                                                                                Application US/08557309E
                                                           6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 amino acids
                                                                                                                                                          Skeiky, Yasir A.V
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206)
                                                                                                                                            Houghton,
                                                                                                                                                                                               Reed, Steven G.
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                                                                            SEED, and BERRY LLP
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                                                                                                                                                                               Yasir A.W.
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                                                                                                                         COMPOUNDS AND METHODS FOR THE DETECTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.48;
                                                                                                                                            Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/403,379A
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Pred. No. 2.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
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NFORMATION FOR SEQ ID NO: 1:
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                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      535 AGQIPAAASVASA-AAVAFSAAAAAVQVAPAAPAPVPAPALVPVPAPAAAQASAPAQTQ 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 ААААТАААІТАТААТІТТТМУАААР---VAVAAAAPA-AAAAPSPATAAATAAAVSPAA 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 ААААААКСКАААКК-----АААРSGKKSAKAAIAPAKAAAAPAKAAAAAAAAA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 AAPAKAATAPAKAAT-APAKA-AAAPAKAATAP 254
                                                                                                                                                                                                                                                                                                                                                                                             ORRESPONDENCE ADDRESS:
                                TELEPHONE:
                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 15-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/557,309B FILING DATE: 14-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Socal Similarity
                                                                                                                                                                                                                                                                                                                                                                             DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAPAKAAAAPAKAATAPAKAAAAPAKTA-AAPAKAAAPAKA-AAAPAKA-ATAPAKAA 22:
                                                                                                                                                                                                                                                                                                                                            Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08929414
                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                       E: SEED and BERRY LLP 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haughton, Raymond
Skeiky, Yasir A.W
                 (206)
                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                        PatentIn
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                                (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steven G.
                682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPOUNDS AND METHODS FOR THE DETECTION OF T. CRUZI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.48;
                                                                                                                                                                                                    Release #1.0,
                                                                                                                                                                    US/08/929,414
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                                                                210121.406C1
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Pred. No. 2.9e-07;
                                                                                                                                                                                                                                                                                                                                                           701 Fifth Avenue
                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
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RESULT; 7
US-08-557-309B-54
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                                                                                                                                            JS-08-557-309B-54
                                                 Where Match 6.2%; Score 209; DB 2; Best Local Similarity 43.7%; Pred. No. 4.2e-07; Matches 69; Conservative 6; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE, ADDRESS:
476 APVAAAATAAAITATAATITTTMYAAAPVAVAAAAAPAAAAAAPSDATAAATA------ 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AAAAPAKAAAAPAKAATAPAKAAAAPAKTA-AAPAKAAAPAKA-AAAPAKA-ATAPAKAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 AAAATAAAITATAATITTMWAAAP----VAVAAAAAPA-AAAAPSPATAAATAAAVSPAA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 AAPAKAATAPAKAAT-APAKA-AAAPAKAATAP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594 APTSAPAVAPTPAPTPTPAVAQAEVPASPATGP 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 AGQIPAAASVASA-AAVAPSAAAAAAVQVAPAAPAPVPAPALVPVPAPAAAQASAPAQTQ 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AAAAAAAKOKAAAKK-----AAAPSGKKSAKAAIAPAKAAAAPAKAAAAPAKAAAAPAK 165
                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                          FILING, DATE:
                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                               219 amino acids
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                                                                                                                                                                                                                                                                 (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houghton, Raymond L.
VENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky, Yasir A.W.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.8e-07;
9; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
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                                                   Indels
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58 AAAAAKOKAAAKKAAAPSGKKSAKAAAP--AKAAAAPAKAAAPPAKTAAAPAKAAAHAKA 115

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: :-09-080-897-2
                                                                                                                                                                                                                                                                           Matches
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (650) 343-434 ORMATION FOR SEQ ID NO:
                                                                                                                                  122
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: MOTTOW, Jan E.
PPLICANT: Welcsh, Piri I.
PPLICANT: Leon, Pedro E.
ITLE OF INVENTION: Modulators of Actin
THEER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116
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                                                                                                                                                                50 VARLQKVETEIQRVSEAYENLVKSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                    7 SSASYQPVP-ADPFAIVSRAQQMV---EILSDENRN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEPHONE:
     EKLEAELATARSTNEDQRRHIEIRDQALSNAQAKVVKL-
                                                                                                                         TSKAGMSQKESSKSAMMYIQELRSGLRDMPLLSCLESLRVSLNNNPVSWVQTFGAEGLAS 181
                                                                                                                                                                                               SSASYGDDPTAQSLQDVSDEQVLVLFEQMLLDMNLNEEKQQPLREKDIIIKREMVSQYLY 12:
                                                                                          LEGEIRRMHDFNRDLRERLETANKQLAEKEYEGSEDTRK----TISQLFAKNKESQREK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAKAAAPPAKAAAPPAKAAAP-PAKAAAP-PAEAAPAP 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAQTQAPTSAPAVAPTPAPTPTPAVAQAEVPASPATGP 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: SCIENCE & TECHNOLOGY LAW GROUP
T: 75 DENISE DRIVE
HILLSBOROUGH
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                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (650)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee, Ming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343-4341
                                                                                                                                                                                                                                                                                         6.28;
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                                                                                                                                                                                                                                                                         95;
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                                                                                                                                                                                                                                                                                         Score 208.5;
Pred. No. 4e
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                -- SKREALEKAMRN-
                                                       -GSYDSRNKHEIIRCLKAFMNNKFG----
                                                                                                                                                                                                                                                                                           4e-06;
                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                       274;
                                                                                                                                                                                                                                                                     Indels 263;
                                                                                                                                                                                                                                                                                                        Length 1248;
   - EEELXKK---
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                                                                                                                                                                --к 87
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                        COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                STREET:
STREET:
STREET:
MA
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                        UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 VAAQRDTTVISHSP-----NTSYDTALEARIQKEEEEILMANKRCLDMEGRIKTLHAQI 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 -QVYVDKVEKMQQAL-----VQLQAAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        743 PEGLTPKKLYKPEV 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 KRDDKSWKGSLGILLGGDYRAEYVPSTPS--PVPPSTPLLSAHSKTGSRDCSTQTERGTE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 IENDAMIKVLQQRSRKEPSKTFQLSCMRPAKSLMSISNAGSGLLSHSSTLTG--SPIMEE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336 QVLQDI.PEIENEDMRVQINVFDEQGEEDSYDIKGRIDDIRMEMDDFNEVFQIII.NTVKDS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 ----RELES--LRIQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ERMEMDEVEREQPILDGLKSGTTIALKVGCLQLINALITPAEELDERVHIRSELMRLGLH 335
                                                                  CLASSIFICATION: . 435
                                                                                                       APPLICATION NUMBER:
                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                             COUNTRY
                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPLPGEAGMPPPPPPLPGGPGIPPPPPPPGGPGIPPPPPGMGMPPPPPFGFGVPAAPVL 742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNKTAAVAPISVPAPVAAAATAAAITATAATITTTMVAAAPVAVAAAAAP--AAAAAPSP 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAEPEFLSILOHLLIVRNDYEARPOYYKLIEECISQIVLHKNGADPDFKCRHLQIEIEGL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDOMIDETKVEKSEAKAAELEKKLDSELTARHELQVEMKKMES----DFEQKLQDLQG-- 510
                                                                                                                                                                                                                                021.09
/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ERILALEADMTKWEQKY--LEENV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08195487
                                                                                                                                                                                                                                                                                                    E: TESTA HURWITE & THIBEAULT 53 STATE STREET
                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                   LIDGARD, GRAHAM F.

VENTION: NOVEL MALIGNANT CELL TYPE MARKERS

VENTION: INTERICE NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKTMLETF::GILLLVRAMDPAVPNMMIDAAKLLSALCILPQPEDMNERVLEAMT
                                                                                                                                                                                                                                                                                                                                                                                                                              TOUKATLY,
                                                                                                                                      PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         636
                                 US/07/901,701
                                                                                                       US/08/195.487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QROGNCQP-
                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---APTPTPAVAQAE-----VPASPAT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----QDLEAEVSQLTGEVAKLTKE 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EKREQLEHRLRTRLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNVSEYNAA -- ALMELLREK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PGDSGT- 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224
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PCT-US93-06160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-195-487-4
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application PC/TUS9306160 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1288 LICGRRCRASGREAEKQRVASENLRQELTSQAERAEELGQELKAWQEKFFQKEQALSTLQ 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1228 SSIEEEVSILNROVLEKEGESKELKRLVMAESEKSOKLEESCACCROROPATVPELONAA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1115 TEPTGPKLEALRAEVSKLEQQCQKQQEQADSLERSLEAERASRAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1056 LTEK-EGKDQELAKLRGLEAAQIKELEELRQTVKQLKEQLAKKEKEHASGSGAQSEAAGR 1114
                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 DMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999 RGQQEREVARLTQERGRAQADLALEKAAR---AELEMRLQNALNEQRVEFATLQEALAHA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 QAKVVKLEEELKKKQ----
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
JRRENT APPLICATION DĀTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 MRNKLEG---EIRRMHDFN-----RDLRERLETANKQLAEKEYE---GS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 RAQQMVEILSDENRNLRQELEGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREALEKA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                               COUNTRY: U
                                                                                                                                                                                                               ADDRESSEE:
STREET: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GELIPLRQKVAEQD---RTAQQLRAEKASYAEQLSMLKKAHGLLAEENRGLG 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEHTSTQALVSELLPAKHLÇQQLQAEQAAAEKRHREELEQSKQAAGGLRAELLRAQREL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDAAATVAAQRDTTVISH--SPNTSYDTALEARIQKEEE-----EILMANKRCL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EM - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGQLEEKAQELGHSQSALASAQRELAAFRTKVQDHSKAEDEWKAQVARGRQEAERKNSLI 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106;
                                                                                                                                                                                           BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PITCHER ESQ,
                                                                                                                                                                         ž
                                                                                                                                                                                                                 E: TESTA HURWITZ & THIBEAUL)
53 STATE STREET
                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      617/248-7100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.1%; Score 204; DB 1; 22.3%; Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                INTERIOR NUCLEAR MATRIX
                                                                                                                                                                                                                                                                                                                  NOVEL MALIGNANT CELL TYPE MARKERS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDMUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27, 829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ELLRE----KEERILALEADMTKWEQKYLE-ENVMRHFA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTP-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ESLRIQQRQGNC-----QPTNVSEYNAAA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VYVDKVEKMQQALVQLQAACEK-REQLEHR--LR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RDSALETL 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŷ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>В</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                              US-09-533-306A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US93-06160-4
                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                        Sequence 2, Application US/08533306A Patent No. 5837457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 6.1%;
Best Local Similarity 22.3%;
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1288 LLCGRRCRASGREAEKQRVASENLRQELTSQAERAEELGQELKAWQEKFFQKEQALSTLQ 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1228 SSLEEEVSILNRQVLEKEGESKELKRLVMAESEKSQKLEESCACCRQRQPATVPELQNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1168 QGQLEEKAQELGHSQSALASAQRELAAFRTKVQDHSKAEDEWKAQVARGRQEAERKNSLI 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1115 TEPTGPKLEALRAEVSKLEQQCQKQQEQADSLERSLEAERASRAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1056 LTEK-EGKDOELAKIRGLEAAQIKELEELRQTVKQIKEQLAKKEKEHASGSGAQSEAAGR 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   334 DMEGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          999 RGQQEREVARLTQERGRAQADLALEKAAR---AELEMRLQNALNEQRVEFATLQEALAHA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 Lм----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 TRLEREL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 MRNKLEG---EIRRMHDFN-----RDLRERLETANKQLAEKEYE---GS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PFILING DATE: 1933621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 RAQQMVEILSDENRNLRQELEGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREALEKA 83
                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                               ~--GELIPLRQKVAEQD----RTAQQLRAEKASYAEQLSMLKKAHGLLAEENRGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDAAATVAAQRDTTVISH--SPNTSYDTALEARIQKEEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAKVVKLEEELKKKQ-------VYVDKVEKMQQALVQLQAACEK-REQLEHR--LR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEHTSTQALVSELLPAKHLCQQLQAEQAAAEKRHREELEQSKQAAGGLRAELLRAQREL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------EDTRKTISQLFAKNKESQREKEKLEAELATARSTNEDQRRHIEIRDQALSNA 173
                   Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PITCHER ESQ,
                                     P.O. Box 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2101 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617,
                                                                                                                                                                              Collins, Francis S. Siciliano, Michael J.
                                                                                                                                                          Claxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                    Harness, Dickey & Pierce, P.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617/248-7000
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                                                                                                                    Rearrangements
                                                                                                                                      Markers for Detection
                                                                                                                                                                David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDMUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELLRE----KEERILALEADMTKWEQKYLE-ENVMRHFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTP-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 204; DB 3;
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ESLRIQQRQGNC-----QPTNVSEYNAAA
                                                                                                                                          of Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163; : Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----EILMANKRCL
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-----RDSALETL 1167

1287

250

286

Gaps

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                                                                                                                   US-08-533-306A-4
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Best Local Similarity
Matches 101; Conserv
                                                                                Sequence 4, Application Patent No. 5837457
                                                                  GENERAL INFORMATION:
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                APPLICANT:
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                                                                                                                                                                                       563
                                                                                                                                                                                                                     393
                                                                                                                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                        276 YLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDM
                                                                                                                                                                                                                                                                                                                                                                                             422
                                                                                                                                                                                                                                                                                                                                                                                                                   216 HRLRTRLERELESLRIQQRQGNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                            372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 IEIRDQALSNAQAKVVKLEEELKKKQ----VYVDKVEKMQQALVQL--QAACEK-REQLE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 TAKENEKKAKSLEADIMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 ELQASEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQLHEYETELEDERNERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 LAAAAKKKLEGDLKDLELQADSAIKGREEAIKQLRKLQAQMKDFQRELEDARASRDEIFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 EILSDENRNLR-----QELEGCYEKVARLQKVETE-----IQRVSEAYENLVKSSKREA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 366 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: September 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAE-----KEYEGS-EDTRKTISQLFA 133
                                                                                                                                                                                                                   SSTLTGSPIME 4C3
                                                                                                                                                                                                                                                                                                                                                                                       ESARQQLERQNKELR-
                                                                                                                                                                                     KSKLRGPPPQE 573
                                                                                                                                                                                                                                                                                    E---GRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSH 392
                                                                                                                                                                                                                                                    EKGNARVKQLKRQLEEAEEESQRINANRRKLQRELDEATESNEA-
                                                                                                                                                                                                                                                                                                                       -LEEQVEQEAREKQAATKSLKQK
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             Liu, Pu
Collins, Francis S.
Siciliano, Michael J.
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Claxton, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DeAnn F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ARIAQLEEELEEEQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKN 421
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                                                                                                   US/08533306A
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Pred. No. 3.5e-06;
4; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                      -SKLHEMEGAVKSKF----KSTIAALEAKIAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---EKEKLEAELATA---RSTNEDQRRH 162
                                                                                                                                                                                                                                                                                                                   -DKKLKEILLQVEDERKMAEQYKEQA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 106;
                                                                                                                                                                                                                                                   -- MGREVNAL 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                      464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311
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US-08-533-306A-4
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: ***
CLASSIFICATION: ***
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
NAME: Smith, Deann F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                         681
872 KSKLRGPPPQE 882
                                 393 SSTLTGSFIME 403
                                                                        820
                                                                                                   336 E---GRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSH 392
                                                                                                                                              773
                                                                                                                                                                                                                                                                                                                            163
                                                                                                                                                                                                                                                                                                                                                        621 TAKENEKKAKSLEADLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRR 680
                                                                                                                                                                                                                                                                                                                                                                                                134 KNKESQR----
                                                                                                                                                                                                                                                                                                                                                                                                                            561 LAAAAKKKLEGDIKDIEIQADSAIKGREEAIKQIRKIQAQMKDFQREIEDARASRDEIFA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 ELQASEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQLHEYETELEDERNERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                  31
                                                                                                                                                                                                                                              216 HRLRTRLERELESIRIQQRQGNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 EILSDENRNLR------QELEGCYEKVARLQKVETE----IQRVSEAYENLVKSSSKREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 LEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAE----KEYEGS-EDTRKTISQLFA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: Septem CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                      EKGNARVKOLKROLEEAEEESQRINANKRKLQRELDEATESNEA
                                                                                                                                          -LEEQVEQEAREKQAATKSLKQK----
                                                                                                                                                                          YLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDM 335
                                                                                                                                                                                                                 ESARQQLERQNKELR-
                                                                                                                                                                                                                                                                                   LE-----ARIAQLEEELEEEQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKN 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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O. Box 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     September 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            641-0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%;
23.4%;
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ber 25, 1995
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Pred. No. 6e-06;
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                                                                                                                                                                                                               -SKLHEMEGAVKSKF----KSTIAALEAKIAQ----
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                                                                                                                                                                                                                                                                                                                                                                                           --EKEKLEAELATA---RSTNEDQRRH 162
                                                                                                                                        DKKLKEILLQVEDERKMAEQYKEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150; Indels 106;
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                                                                    MGREVNAL
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393 SSTLTGSPIME 403

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              163 IEIRDQALSNAQAKVVKLEEELKKKQ-----VYVDKVEKMQQALVQL--QAACEK-REQLE 215
                                                                                                                                                                                                                                                  552 TAKENEKKAKSLEADLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRR
                                                                                                                                                                                                                                                                                                                         492 LAAAAKKKLEGDLKDLELQADSAIKGREEAIKQLRKLQAQMKDFQRELEDARASRDEIFA 551
                                                                                                                                                                                                                                                                                                                                                                                               432 ELQASEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQLHEYETELEDERNERA 491
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                                                                            276
                                                                                                                                                                                                                                                                                               134 KNKESQR----
                                       704 -LEEQVEQEAREKQAATKSLKQK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Siciliance APPLICANT: Claxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           80 LEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAE----KEYEGS-EDTRKTISQLFA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                30 EILSDENRNLR-----QELEGCYEKVARLQKVETE----IQRVSEAYENLVKSSSKREA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, Deann F. REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
E---GRIKTLHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSH 392
                                                                       YLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDM
                                                                                                            ESARQQLERQNKELR----
                                                                                                                                            HRLRTRLERELESLRIQORQGNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQK 275
                                                                                                                                                                            LE-----ARIAQLEEELEEEQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKN 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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Siciliano, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (810) 641-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08533306A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
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                                                                                                           -----SKLHEMEGAVKSKF----KSTIAALEAKIAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 203; DB 2;
Pred. No. 5.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2115-00869СОВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                     ---EKEKLEAELATA---RSTNEDQRRH 162
                                   -DKKLKEILLQVEDERKMAEQYKEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 816;
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US-08-742-923A-2
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                                                                                                                                                                                                                                                                                                                                         Matches 101;
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (810) 641-02
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 2:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Smith; Deann F.
REGISTRATION NUMBER: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               163 IEIRDQALSNAQAKVVKLEEELKKKQ-----VYVDKVEKMQQALVQL--QAACEK-REQLE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                  312 TAKENEKKAKSLEADLMQLQEQLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRR 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
            216 HRLRTRLERELESLRIQQRQGNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQK 275
                                                                                                                                                           134 KNKESQR. ----
                                                                                                                                                                                        252 LAAAAKKKLEGDLKDLELQADSAIKGREEAIKQLRKLQAQMKDFQRELEDARASRDEIFA 311
                                                                                                                                                                                                                                                             192 ELQASEDAKLRLEVNMQALKGQFERDLQARDEQNEEKRRQLQRQLHEYETELEDERNERA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: Markers for De ITLE OF INVENTION: Rearrangements
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                                                                                                                                                                                                                      80 LEKAMRNKLEGEIRRMHDFNRDLRERLETANKQLAE-----KEYEGS-EDTRKTISQLFA 133
                                                                                                                                                                                                                                                                                                30 EILSDENRNLR-----QELEGCYEKVARLQKVETE-----IQRVSEAYENLVKSSSKREA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: No. 51 CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 48303
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Bloomfield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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O. Box 828
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                                                --ARIAQLEEELEEEQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/742,923A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36683
                                                                                                                                                                                                                                                                                                                                       74;
                                                                                                                                                                                                                                                                                                                                                       Score 203;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2115-00869DVC
                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version
                                                                                                                                                         --EKEKLEAELATA---RSTNEDQRRH 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P.L.C.
                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                   150; Indels 106;
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                                                                                                                                                                                                                                                                                                                                                                      Length 576
                                                                                                                                                                                                                                                                                                                                 Gaps
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134 KNKESQR	80 LEKAMRNKLEGEIRRMHDENRDLRERLETANKQLAEKEYEGS EDTRKTISQLFA	30 EILSDENRNLRQELEGCYEKVARLQKVETEIQRVSEAYENLVKSSSKREA	Query Match 6.1%; Score 203; DB 2; Length 885; Best Local Similarity 23.4%; Pred. No. 6e-06; Matches 101; Conservative 74; Mismatches 150 Indels 106; Gaps	TOPOLOGY: linear MOLECULE TYPE: protein -08-742-923A-4	LENGTH: 885 amino acids TYPE: amino acid	NICATION INFORMATION: (810) 641-16: (810) 641-0270	Q 🛪	APPLICATION NUMBER: US/08/742,923A FILING DATE: No. 5869611ember 1, 1996 CLASSIFITATION: 416	DA n	IBM PC C	18	COUNTRY: USA	P.O. Box 828 Bloomfield Hills	DENCE ADDRESS, EE: Harness,	TITLE OF INVENTION: MARKETS FOR Detection of Chromosome 16 TITLE OF INVENTION: Rearrangements NUMBER OF SEQUENCES: 14	CANT: Siciliano, Michael J. CANT: Claxton, David	Collins, Francis S	Sequence 4, Application US/08742923A ent NO. 5869611 MERAL INFORMATION:	RESULT 15 US-08-742-923A-4	563 KSKLRGPPPQE 573	393 SSTLTGSPIME 403	511 EKGN	336 EGRIKTLHAQIIEKDAMIKVLQQRSRKEPSKT	276 YLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDM	422 ESARQQLERQNKELRSKLHEMEGAVKSKFKSTTAALEAKIAQ
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		393 SSTLTGSPINE 403	QY.	
	871	820 EKGNARVKQLKRQLEEAEEESQRINANRRKLQRELDEATESNEAMGREVNAL 871	ממ	
	392	336 EGRIKTIHAQIIEKDAMIKVLQQRSRKEPSKTEQLSCMRPAKSLMSISNAGSGLLSH 392	Οv	
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٠.	335	276 YLEENVMRHFALDAAATVAAQRDTTVISHSPNTSYDTALEARIQKEEEEILMANKRCLDM 335	· Qy	
	773	731 ESARQQLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQ 773	ρb	
	275	215 HRLRTRLERELESLRIQQRQGNCQPTNVSEYNAAALMELLREKEERILALEADMTKWEQK 275	ą	
	730	531 LEARIAQLEEELEEEQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKN 730	B	
	215	163 ICIKLQALSNAQAKVVKLEEELKKKQVYVDKVEKMQQALVQLQAACEK-REQLE 215	Qy VQ	
	089	621 TAKENEKKAKSLEADLMOLOEDLAAAERARKQADLEKEELAEELASSLSGRNALODEKRR 680	Dio	

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